

SEQUENCE LISTING

<110> SmithKline Beecham Biologicals S.A.

<120> Novel Compounds

<130> BM45351

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2169

<212> DNA

<213> *Neisseria meningitidis*

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cagcgttcgt acaacgcgat tgtcaccgag aaaaacggcg attacagctc gtttgccgtc	180
accgtcggca caaaaatccc cgcttctttg cgcgaaattc cgcaatccgt cagtatcatc	240
accaaccagc aggtcaaaga ccgcaatgtt gatacgtttg accagttggc gcgcaaaacg	300
ccgggcctgc gcgtgttgag caacgatgac ggacgctctt cggtttacgc gcgcgggttac	360
gaatacagcg aatacaacat cgacggcctg cccgcgcaga tgcagagtat caacggcacg	420
ctgcccattc tggttcgcctt cgaccgcgtg gaagtgatgc gcggggccgag cggactgttc	480
gacagcagcg gcgagatggg cggtatcgtg aatctggtgc gcaaacgccc gaccaaagcg	540
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gtatcgggca gcctcaattc agacggcagc gtgcgcggcc gcgtgatggc gcagaccgtc	660
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<210> 2

<211> 722

<212> PRT

<213> *Neisseria meningitidis*

<400> 2

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 35 40 45
 Thr Glu Lys Asn Gly Asp Tyr Ser Ser Phe Ala Val Thr Val Gly Thr
 50 55 60
 Lys Ile Pro Ala Ser Leu Arg Glu Ile Pro Gln Ser Val Ser Ile Ile
 65 70 75 80
 Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln Leu
 85 90 95
 Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly Arg
 100 105 110
 Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile Asp
 115 120 125
 Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn Leu
 130 135 140

Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu Phe
 145 150 155 160
 Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys Arg
 165 170 175
 Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr His
 180 185 190
 Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser Asp
 195 200 205
 Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser Pro
 210 215 220
 Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala Ala
 225 230 235 240
 Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu Tyr
 245 250 255
 Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala Asn
 260 265 270
 Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp Trp
 275 280 285
 Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys His
 290 295 300
 Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser Asp
 305 310 315 320
 Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly Met
 325 330 335
 Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys Ala
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 Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala Phe
 355 360 365
 Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn Glu
 370 375 380
 Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu Gln
 385 390 395 400
 Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu Phe
 405 410 415
 Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly Val
 420 425 430
 Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe Gly
 435 440 445
 Ile Tyr Gly Lys Ser Thr Phe His Pro Ala Asp Gly Leu Ser Leu Ile
 450 455 460
 Gly Gly Gly Arg Leu Gly His Tyr Lys Ile Glu Ser Gly Glu Gly Lys

465		470		475		480
Thr Leu His Lys Ala Ser Lys Thr Lys Phe Thr Gly Tyr Ala Gly Ala						
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Val Tyr Asp Leu Asn Asp Asn Asn Ser Leu Tyr Leu Ser Leu Ser Gln						
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Leu Tyr Thr Pro Gln Thr Asn Leu Asp Ala Asp Gly Lys Leu Leu Lys						
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Pro Arg Gln Gly Asn Gln Phe Glu Val Gly Tyr Lys Gly Ser Tyr Met						
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Asp Asp Arg Leu Asn Ala Arg Val Ser Phe Tyr Arg Met Lys Asp Lys						
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Asn Ala Ala Ala Pro Leu Asn Pro Asn Asn Lys Lys Thr Arg Tyr Ala						
	565			570		575
Ala Leu Gly Lys Arg Val Met Glu Gly Val Glu Thr Glu Ile Ser Gly						
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Ala Val Thr Pro Lys Trp Gln Ile His Ala Gly Tyr Ser Tyr Leu His						
	595			600		605
Ser Gln Ile Lys Thr Ala Ser Asn Ser Arg Asp Asp Gly Ile Phe Leu						
610		615			620	
Leu Met Pro Lys His Ser Ala Asn Leu Trp Thr Thr Tyr Gln Val Thr						
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Pro Glu Leu Thr Ile Gly Gly Gly Val Asn Ala Met Ser Gly Ile Thr						
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Ser Ser Ala Gly Met His Ala Gly Gly Tyr Ala Thr Phe Asp Ala Met						
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Ala Ala Tyr Arg Phe Thr Pro Lys Leu Lys Leu Gln Ile Asn Ala Asp						
	675			680		685
Asn Ile Phe Asn Arg His Tyr Tyr Ala Arg Val Gly Gly Ala Asn Thr						
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Phe Asn Ile Pro Gly Ser Glu Arg Thr Trp Thr Ala Asn Leu Arg Tyr						
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<210> 3

<211> 2078

<212> DNA .

<213> *Neisseria meningitidis*

<400> 3

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 cgatggcggc ataccgcttc acgcccagc tgaagctgca aatcaacgcc gacaacatct 1980
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<210> 4

<211> 691

<212> PRT

<213> *Neisseria meningitidis*

<400> 4

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 35 40 45
 Ile Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln
 50 55 60
 Leu Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly
 65 70 75 80
 Arg Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile
 85 90 95
 Asp Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn
 100 105 110
 Leu Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu
 115 120 125
 Phe Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys
 130 135 140
 Arg Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr
 145 150 155 160
 His Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser
 165 170 175
 Asp Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser
 180 185 190
 Pro Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala
 195 200 205
 Ala Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu
 210 215 220
 Tyr Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala
 225 230 235 240
 Asn Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp
 245 250 255
 Trp Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys
 260 265 270
 His Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser
 275 280 285
 Asp Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly
 290 295 300
 Met Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys
 305 310 315 320
 Ala Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala

325 330 335
 Phe Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn
 340 345 350
 Glu Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu
 355 360 365
 Gln Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu
 370 375 380
 Phe Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly
 385 390 395 400
 Val Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe
 405 410 415
 Gly Ile Tyr Gly Lys Ser Thr Phe His Pro Ala Asp Gly Leu Ser Leu
 420 425 430
 Ile Gly Gly Gly Arg Leu Gly His Tyr Lys Ile Glu Ser Gly Glu Gly
 435 440 445
 Lys Thr Leu His Lys Ala Ser Lys Thr Lys Phe Thr Gly Tyr Ala Gly
 450 455 460
 Ala Val Tyr Asp Leu Asn Asp Asn Asn Ser Leu Tyr Leu Ser Leu Ser
 465 470 475 480
 Gln Leu Tyr Thr Pro Gln Thr Asn Leu Asp Ala Asp Gly Lys Leu Leu
 485 490 495
 Lys Pro Arg Gln Gly Asn Gln Phe Glu Val Gly Tyr Lys Gly Ser Tyr
 500 505 510
 Met Asp Asp Arg Leu Asn Ala Arg Val Ser Phe Tyr Arg Met Lys Asp
 515 520 525
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 530 535 540
 Ala Ala Leu Gly Lys Arg Val Met Glu Gly Val Glu Thr Glu Ile Ser
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 Gly Ala Val Thr Pro Lys Trp Gln Ile His Ala Gly Tyr Ser Tyr Leu
 565 570 575
 His Ser Gln Ile Lys Thr Ala Ser Asn Ser Arg Asp Asp Gly Ile Phe
 580 585 590
 Leu Leu Met Pro Lys His Ser Ala Asn Leu Trp Thr Thr Tyr Gln Val
 595 600 605
 Thr Pro Glu Leu Thr Ile Gly Gly Gly Val Asn Ala Met Ser Gly Ile
 610 615 620
 Thr Ser Ser Ala Gly Met His Ala Gly Gly Tyr Ala Thr Phe Asp Ala
 625 630 635 640
 Met Ala Ala Tyr Arg Phe Thr Pro Lys Leu Lys Leu Gln Ile Asn Ala
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Asp Asn Ile Phe Asn Arg His Tyr Tyr Ala Arg Val Gly Gly Ala Asn
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Tyr Ser Phe
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<220>
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30

<210> 6
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<220>
<223> Primer

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33